

1	MASTTPITME	DLQKALEAQS	RALRAGLAAG	ASQSRPRPP	RHARLQHLPE	50
51	MTPAVTPEGP	APPRTGAWQR	KOWSRAPPPP	EERQESRSQT	PAPKPSRAPP	100
101	QPOPPRMOT	GRGGSAPRPE	LCPPTNPFQA	AVARGLRPPL	HOPOTEAPTE	150
151	ACVTSWLWSE	GEGAVFYRVD	LHFINLGTPP	LDODGRWOPA	LMYNPCGPEP	200
201	PAHVVRAYNQ	PAGOVYGVWG	KGERTYAEQD	FRVGGTRWHR	LLRMPVRGLD	250
251	GOTAPLPPTH	TERIETRSAR	HPWRIRFGAP	CAFLAGLLLA	AVAVGTARAG	300
301	LQPRADMAAP	PMPPQPPRAH	GQHYGHHHQ	LPFLGHDGHH	GGTLRVGQHH	350
351	RNASOVLPGH	WLQGGNGCYN	LSDWHQGTHV	CHTKHMDPNC	VEHORPPPAT	400
401	PTSLTTAANY	IAAATPATAP	PPCHAGLNDS	CGGFLSGCGP	MRLPTALTGP	450
451	AVGDLRAVHH	RPVPAYPVCC	AMRWGLPPWE	LVILTARPED	GWTCRGVPAH	500
501	PGTRCPELYS	PMGRATCSPA	SALWLATANA	LSLDHAFAAF	VLLVPMVLIF	550
551	MVCRRACRRP	APPPSPQSS	CRGTTTPPAYG	EEAFTYLCTA	PGCATOTVVP	600
601	VRLAGVGFES	KIVDGGCFAP	MOLEATGACI	CEIPTOVSCE	GLGAWPTAP	650
651	CARIWNGTOR	ACTFWAVNAY	SSGGYAOLAS	YFNPGGSYYK	OYHPTACEVE	700
701	PAFGHSDAAC	WGFPDTVMS	VFALASYVOH	PHKTVRVKFK	TETRTVMOLS	750
751	VAGVSCNVTT	EHPFCNTPHG	QLEVQVPPDP	GOLVEYIMNY	TGNQQSRWGL	800
801	GSPNCHGPDW	ASPVCQRHSP	DCSRLVGATP	ERPRLRLVDA	DDPLLRTAPG	850
851	PGEVMTVPYI	GSOARKCGLH	IRAGPYGHAT	YEMPEWIAH	TTSDPMHPPG	900
901	PLGLKFKTYR	PVALPRALAP	PRNVRVTGCT	QCGTPALVEG	LAPGGGNCHL	950
951	TVNGEDVGAF	PPGKFVTAAL	LHTPPPYQVS	CGGESDRASA	GH.....	1000

FIGURE 1

5 10 15 20 25 30
 1 M A S T T P M E D L Q K A L E A Q S R A A E L A A G
 31 A S Q S R R P P P R Q R D S S T S G D D S G R D S G G P R
 61 R R R G N R G R G Q R R D W S R A P P P P E E R Q E S R S
 91 ~~T P A P P R~~ S R A P P Q Q P P P R M Q T G R G G S A P R P
 121 E L G P P T N P F Q A A V A R G L R P P L H D P D T E A P T
 151 E A C V T S W L W S E G Q G A V F Y R V D L H F T N L G T P
 181 P L D E D G R W D P A L M Y N P C G P E P P A H V V R A Y N
 211 Q P A G D V R G V W G K G E R T Y A E Q D F R V G G T R W H
 241 R L L R M P V R G L D G D S A P L P P H T T E R I E T R S A
 271 R H P W R I R F G A P Q A F L A G L L L A T V A V G T A R A
 301 G L Q P R A D M A A P P T L P P P R ^{CH} H G Q H Y G H H H H
 331 Q L P F L G H D G H H G G T L R V G Q H Y R N A S D V L P G
 361 H W L Q G G W G C Y N L S D W H Q G T H V C H T K H M D E W
 391 C V E H A R P P P A T P T P L T T A A N S T T A A T P A T A
 421 P A P C H A G L N D S C G G F L S G C G P M R L R H G A D T
 451 R C G R L I C G L S T T A Q Y P P T R F G C A M R W G L P P
 481 W E L V V L T A R P E D G W T C R G V P A H P G A R C P E L
 511 V S P M G R A T C S P A S A L W L A T A N A L S L D H A L A
 541 A F V L S V P W V L I F M V C R R A C R R R G A A A A L T A
 571 V V L Q G Y N P P A Y G E E A F T Y L C T A P G C A T Q A P
 601 V P V R L A G V R F E S K I V D G G C F A P W D L E A T G A
 631 C I C E I P T D V S C E G L G A W V P A A P C A R I W N G T
 661 Q R A C T F W A V N A Y S S G G Y A Q L A S Y F N P G G S Y
 691 Y K Q Y H P T A C E V E P A F G H S D A A C W G F P T D T V
 721 M S V F A L A S Y V Q H P H K T V R V K F H T E T R T V W Q
 751 L S V A G V S C H V T T E H P F C H T P H G Q L E V Q V P P
 781 D P G D L V E Y I M N Y T G N Q Q S R W G L G S P N C H G P
 811 D W A S P V C Q R H S P D C S R L V G A T P E R P R L R L V
 841 D A D D P L L R T A P G P G E V W V T P V I G S Q A R K C G
 871 L H I R A G P Y G H A T V E M P E W I H A H T T S D P W H P
 901 P G P L G L K F K T V R P V A L P R T L A P P R N V R V T G
 931 C Y Q C G T P A L V E G L A P G G G N C H L T V N G E D V G
 961 A V P P G K F V T A A L L N T P P P Y Q V S C G G E S D R A
 991 S A R V I D P A A Q S F T G V V Y G T H T T A V S E T R Q T
 1021 W A E W A A A H W W Q L T L G A T C A L P L A G L L A C C A
 1051 K C L Y Y L R G A I A P R

FIGURE 2

1 M A S T T P I T M E D L Q K A L E A Q S R A L R A E L A A G
 31 A S Q S R R P R P P R Q R D S S T S G D D S G R D S G G P R
 61 R R R G N R G R G Q R R D W S R A P P P P E E R Q E S R S
 91 T P A P P R S R A P P Q Q P P P R M Q T G R G G S A P R P
 121 E L G P P T H P F Q A A V A R G L R P P L H D P D T E A P T
 151 E A C V T S W L W S E G Q G A V F Y R V D L H F T N L G T P
 181 P L D E D G R W D P A L M Y N P C G P E P P A H V V R A Y N
 211 Q P A G D V R G V W G K G E R T Y A E Q D F R V G G T R W H
 241 R L L R M P V R G L D G D S A P L P P H T T E R I E T R S A
 271 R H P W R I R F G A P Q A F L A G L L L A T V A V G T A R A
 301 G L Q P R A D M A A P P T L P Q P P R A H G Q H Y G H H H H
 - 331 Q L P F L G H D G H H G G T L R V G Q H Y R N A S D V L P G
 361 H W L Q G G W G C Y N L S D W H Q G T H V C H T K H M D F W
 391 C V E H A R P P P A T P T P L T T A A N S T T A A T P A T A
 421 P A P C H A G L N D S C G G F L S G C G P M R L R H G A D T
 451 R C G R L I C G L S T T A Q Y P P T R F G C A M R W G L P P
 481 W E L V V L T A R P E D G W T C R G V P A H P G A R C P E L
 511 V S P M G R A T C S P A S A L W L A T A N A L S L D H A L A
 541 A F V L S V P W V L I F M V C R R A C R R R G A A A A L T A
 571 V V L Q G Y N P P A Y G E E A F T Y L C T A P G C A T Q A P
 601 V P V R L A G V R F E S K I V D G G C F A P W D L E A T G A
 631 C I C E I P T D V S C E G L G A W V P A A P C A R I W N G T
 661 Q R A C T F W A V N A Y S S G G Y A Q L A S Y F N P G G S Y
 691 Y K Q Y H P T A C E V E P A F G H S D A A C W G F P T D T V
 721 M S V F A L A S Y V Q H P H K T V R V K F H T E T R T V W Q
 751 L S V A G V S C N V T T E H P F C N T P H G Q L E V Q V P P
 781 D P G D L V E Y I M N Y T G N Q Q S R W G L G S P N C H G P
 811 D W A S P V C Q R H S P D C S R L V G A T P E R P R L R L V
 841 D A D D P L L R T A P G P G E V W V T P V I G S Q A R K C G
 871 L H I R A G P Y G H A T V E M P E W I H A H T T S D P W H P
 901 P G P L G L K F K T V R P V A L P R T L A P P R N V R V T G
 931 C Y Q C G T P A L V E G L A P G G G N C H L T V N G E D V G
 961 A V P P G K F V T A A L L N T P P P Y Q V S C G G E S D R A
 991 S A R V I D P A A Q S F T G V V Y G T H T T A V S E T R Q T
 1021 W A E W A A A H W W Q L T L G A T C A L P L A G L L A C C A
 1051 K C L Y Y L R G A I A P R

FIGURE 2

	10	20	30	40	50	
1	MGARASVLSG	GELDRWEKIR	LRPGGKKKYK	LKHIVWASRE	LERFAVNPGL	50
	60	70	80	90	100	
51	LETSEGCROI	LGQLQPSLQT	GSEELRSLYN	TVATLYCVHQ	RIEIKOTKEA	100
	110	120	130	140	150	
101	LKIEEEQNK	SKKKAQAAA	DTGHSSQVSQ	NYPIVQNIQG	QMVHQAI SPR	150
	160	170	180	190	200	
151	TLN A WVKVVE	EKA F SPEVIP	MFSALSEGAT	PQDLNTMLNT	VGGHQAAMQM	200
	210	220	230	240	250	
201	LKETINEEAA	EWDRVHPVHA	GPIAPQMRE	PRGSDIAGTT	STLQEIQGNM	250
	260	270	280	290	300	
251	TNNPPIPVGE	IYKRWIILGL	NKIVRMYSPT	SILDIROGPK	EPFRDYVDRF	300
	310	320	330	340	350	
301	YKTLRAEQAS	QEVKNWMTET	LLVQANPDC	KTILKALGPA	ATLEEMMTAC	350
	360	370	380	390	400	
351	QGVGGPGHKA	RVLA E AMSQV	TNTATIM M QR	GNFRNQRKMV	KCFNCGKEGH	400
	410	420	430	440	450	
401	TARNCRAPRK	KGCN K CGKEG	HQMKDOCTERQ	ANFLGKICLP	TREGQGIFFR	450
	460	470	480	490	500	
451	ADQSQQPHHF	FRADQSQQPH	QKRASGLG..	500

FIGURE 3

	20	30	40	50		
1	MRVKEKYOHL	WRWGKWKGTM	LLGILMCSA	TEKLWYTVYY	GVPVWKEATT	50
	60	70	80	90	100	
51	TLFCASDAKA	YDEVHNVWA	THACVPTDPN	POEVVLNVNT	ENFNMWKNOM	100
	110	120	130	140	150	
101	VEQMHEDIIS	LWDQSLKPCV	KLTPLCVSLK	CTDLGNATNT	NSSNTNSSSG	150
	160	170	180	190	200	
151	EMMMEKGEIK	NCSFNISTSI	RGKVQKEYAF	FYKLDIIPID	NOTTSYTLTS	200
	210	220	230	240	250	
201	CNTSVITQAC	PKVSFEPIPI	HYCAPAGFAI	LKCNKTFNG	TGPCTNVSTV	250
	260	270	280	290	300	
251	QCTHGIRPVV	STQLLNGSL	AEDEVVIRSA	NFTDNAKTII	VQLNQSVEIN	300
	310	320	330	340	350	
301	CTRPNNNTRK	SIRIQRGPR	AFVTICKIGH	MROAHCNISR	AKWNATLKQI	350
	360	370	380	390	400	
351	ASKLREQFGN	NKTIIFKOSS	GGDPEIVTMS	FNCGGEFFYC	NSTQLFNSTW	400
	410	420	430	440	450	
401	FNSTWSTEGS	NNTEGSDTIT	LPCRICKQFIN	MWOEVGKAMY	APPISGQIRC	450
	460	470	480	490	500	
451	SSNITGLLLT	RDGGNNNNGS	EIFRPGGGDM	RONWRSELYK	YKVVKIEPLG	500
	510	520	530	540	550	
501	VAPTAKRRV	VQREKRAVGI	GALFLGFLGA	AGSTMGARSM	TLTVQARQLL	550
	560	570	580	590	600	
551	SGIVQQQNNL	LRAIEAQQL	LQLTVWGIKQ	LQARILAVER	YKDOQQLGI	600
	610	620	630	640	650	
601	WGCSGKLICT	TAVPWNASWS	NKSLEQIWN	MTWMEWOREI	NNYTSLIHSL	650
	660	670	680	690	700	
651	IEESQNNQEK	NEOELLELDK	WASLWNNFNI	TNWLWYIKIF	IMIVGGLVGL	700
	710	720	730	740	750	
701	RIVFAVLSIV	NRVRQGYSP	SFQTHLPTPR	GPDRPEGIEE	EGGERDRDRS	750
	760	770	780	790	800	
751	IRLVNGSLAL	IWOOLRSCL	FSYHRLRDL	LIVTRIVELL	GRRGWEALKY	800
	810	820	830	840	850	
801	WNNLLQYWSQ	ELKNSAVSLL	NATAIAVAEG	TORVIEVVQG	ACRAIRHIPR	850
	860	870	880	890	900	
851	RIRQGLERIL	L				900

FIGURE 4

	10	20	30	40	50	
1	MKTTLKMTAL	AALSAFVLG	CGSHOMKSEE	HANMQLQQQA	VLGLNWMQDS	50
	60	70	80	90	100	
51	GEYKALAYQA	YNAAKVAFDH	AKVAKGKKKA	VVAOLDETML	DNSPYAGHOV	100
	110	120	130	140	150	
101	<u>QNNKPF</u> DGKO	WTRWVDARQS	RAVPGAVEFN	NYVNSHNGKV	FYVTNRKDST	150
	160	170	180	190	200	
151	EKSGTIDDMK	RLGFNGVEES	AFYLKKOKSA	KAARFAEIEK	QGYEIVLYVG	200
	210	220	230	240	250	
201	DNLDDFGNTV	YGKLNADRRR	FVDONQGKFG	KTFIHLPNAN	YGGWEGGLAE	250
	260	270	280	290	300	
251	GYFKKDTQGQ	IKARLOAVQA	WOGK.....	300

FIGURE 5

	10	20	30	40	50	
1	<u>IQPPKNLLFS</u>	SLLFSSLLFS	SAAQAASEDR	RSPYYVQADL	AYAAERITHD	50
	60	70	80	90	100	
51	YPQATGANNT	STVSDYFRNI	RAHSIHPRVS	VGYDFGGWRI	AADYASYRKN	100
	110	120	130	140	150	
101	NNNKYSVNTK	ELENKHNNKK	DLKTENQENG	TFHAASSLGL	SAIYDFKLKG	150
	160	170	180	190	200	
151	KFKPYIGARV	AYGHVRHSID	200

FIGURE 6

.....KLMI*K

6

	10	20	30	40	50	
7	FVTKM*YKTL	DKYLRRRLIL	NISIV*K*LS	EKR*I*MNKK	KMILTSLASV	56
	60	70	80	90	100	
57	AILGAGFYAS	QPTVVRAEES	PVASQSKAEK	OYDAAKKDAK	NAKKAVEDAQ	106
	110	120	130	140	150	
107	KALDDAKAAQ	KKYDEDOKKT	EEKAALKAA	SEEMDKAVAA	VQQAYLAYQQ	156
	160	170	180	190	200	
157	ATDKAAKDAA	OKMIDEAKKR	EEAKTKFNT	VRAMVPEPE	QLAETKKKSE	206
	210	220	230	240	250	
207	EAKQKAPILT	KKLEEAKAKL	EEAEKKATEA	KQKVDAEEVA	PQAKIAELEN	256
	260	270	280	290	300	
257	QVHRLEQELK	EIDSESEEDY	AKEGFRAPLQ	SKLDAKKAKL	SKLEELSDKI	306
	310	320	330	340	350	
307	DELDAAEIAKL	EDOLKAAEEN	NNVEDYFKEG	LEKTIAAKKA	ELEKTEADLK	356
	360	370	380	390	400	
357	KAVNEPEKPA	PAPETPAPEA	PAEQPKPAPA	PQPAPAPKPE	KPAEQPKPEK	406
	410	420	430	440	450	
407	TDDQQAEEEDY	ARRSEEEYNR	LTQQQPPKAE	KPAPAPKTGN	KQENGMYFY	456
	460	470	480	490	500	
457	NTDGSMTAGN	LQNGSNYYL	NSNGAMATGN	LQYNGSNYYL	NANGAMATGN	506
	510	520	530	540	550	
507	AKVNGSNYYL	NANGAMATGN	LQYNGSNYYL	NANGAMATGN	AKVNGSNYYL	556
	560	570	580	590	600	
557	NANGAMATGN	LOYNGSNYYL	NANGAMATGN	AKVNGSNYYL	NANGAMATGN	606
	610	620	630	640	650	
607	VKDGOTWYYL	EASGAMKASQ	WFKVSDKWYY	VHGLGALAVN	TTYDGYKVNA	656
	660	670	680	690	700	
657	NGEW*AD*I	KAC*EHLTF*	F*NKDKVRLN	RFMFVFFRY.	706

FIGURE 7

	10	20	30	40	50	
1	MMMKKATIAA	TAGIAVTAFR	APTIRSASTV	VVEAGDTLWG	IAQSKGTTVO	50
	60	70	80	90	100	
51	AIKKANNLTT	OKIVPGOKLQ	VNNEVAAA EK	TEKSVSATWL	NVRSGAGVON	100
	110	120	130	140	150	
101	SIITSIKGGT	KVTVETTESN	GWHKITYNOG	KTGFVNGKYL	TDKAVSTPVA	150
	160	170	180	190	200	
151	<u>PTQEVKKETT</u>	TQQAAPAAET	KTEVKQTTQA	<u>TTPAPKVAET</u>	KETPVVQQNA	200
	210	220	230	240	250	
201	TTHAVKSGDT	IWALSVKYGV	SVQDIMSNN	LSSSSIVVGQ	KLAIKQTANT	250
	260	270	280	290	300	
251	<u>ATPKAEVKTE</u>	APAAEKQAAP	VVKENTNTNT	ATTEKKETAT	<u>QQQTAPKAPT</u>	300
	310	320	330	340	350	
301	EAAKPAPAPS	TNTNANKTNT	NTNTNTNTNN	TNTNTPSKNT	NTNSNTNTNT	350
	360	370	380	390	400	
351	NSNTNANQGS	SNNNSNSSAS	AIIAEAQKHL	GKAYSWGNG	PTTFDCSGYT	400
	410	420	430	440	450	
401	KYVFAKAGIS	LPRTSGAQYA	STTRISESQA	KPGDLVFFDY	GSGISHVGIY	450
	460	470	480	490	500	
451	VGNGQMINAQ	DNGVKYDNIH	GSGNGKYLVG	FGRV.....	500


FIGURE 8

	10	20	30	40	50	
1	
	MKVS	AALLCL	LLIAATFI	PQGLAQPD	AINA PVTCCYNFTN	RKISVQRLAS 50
	60	70	80	90	100	
51	YRRITSSKCP	KEAVIFKTI	VAKEICADPKQ	KWVQDSMOHL	OKQTQTPKT.	100

FIGURE 9

	10	20	30	40	50	
1	
	KSTTCCYRFI	NKKIPKORLE	SYRRTTSSHC	PREAVIFKDK	EICADPTOKW	50
	60	70	80	90	100	
51	VQDFMKHLDK	<u>KTQTPKL</u>	100

FIGURE 10

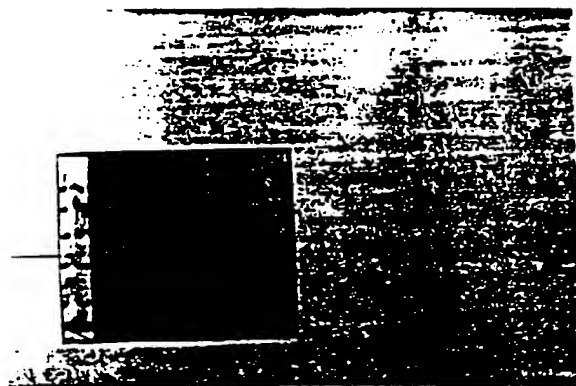


1 2/3 4/5/6 7/8 9/10

Immunoblots of RV antigens reacted with Mab's RV1, RV2, RV3 and RV4. RV antigen: Strain MPV-77 (lot# 50678, Catalogue # EL-05-04) cultured in Vero cells. Purchased from Microbix Biosystems Inc., Toronto, Ontario. All Mab used as tissue culture fluid diluted 1/500.

Lane 1 - Molecular weight markers of 97, 66, 45, 31, 21, and 14kD. Lane 2/3 - RV4; Lane 4/5/6 - RV3; Lane 7/8 - RV2; Lane 9/10 - RV1. Lanes 2-9 all illustrate two proteins, 31 kD (major) and 45 kD (minor), identified by reaction with Mab's 1-4.

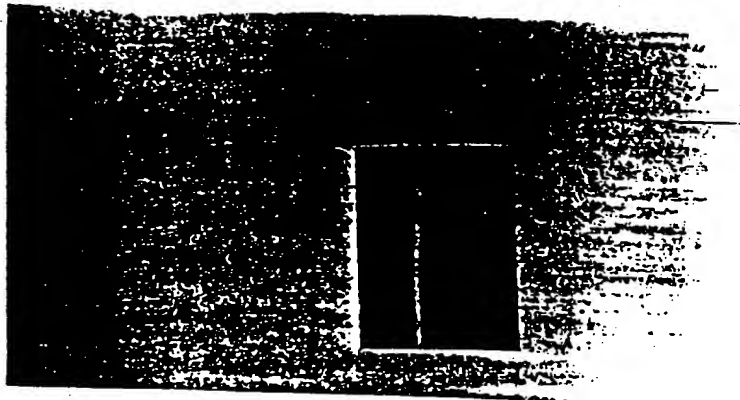
FIGURE 11



1 2 3 4/5 6/7

Immunoblots of bacterial antigens reacted with RV Mab RV1.
H. Influenzae b antigen from ATCC (#10211); **L. monocytogenes** from ATCC (#7644); **S. pneumoniae** from the Caribbean Regional Epidemiology Centre, CAREC, Trinidad; **N. meningitidis** A from ATCC #13077.
 Lane 1 - Molecular weight markers of 97, 66, 45, 31, 21, and 14 kD.
 Lane 2 - **H. Influenzae** b - proteins of approximate weights of 50, 45, 40, and 25 kD.
 Lane 3 - **L. monocytogenes** - proteins of approximate weights of 60 kD (major) and 66 kD (minor).
 Lane 4/5 - **S. pneumoniae** - proteins of approximate weights of 60 kD and 66 kD.
 Lane 6/7 - **N. meningitidis** - a protein of approximate weights of 13 kD, identified by reaction with Mab RV1.

FIGURE 12



1 2 3/4

Immunoblots of HIV1 antigens reacted with RV Mab RV1.
HTLV-IIIIB viral lysate, lot #54-040, purchased from Applied
Biotechnologies, Inc., Md., USA.
Lane 1 - Molecular weight markers of 97, 66, 45, 31, 21, and 14 kD.
Lane 2 - Control RV antigens, 31 and 45 kD, reacting with RV1 Mab.
Lane 3/4 - HIV1 antigen of approximate weights of proteins at 24 kD
and 61 kD, identified by reaction with Mab RV1.

FIGURE 13